

RAW SEQUENCE LISTING

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Application Serial Number: 10/551, 655A
Source: IFWP
Date Processed by STIC: 10/12/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/551,655A

TIME: 09:38:14

Input Set : A:\80621031.APP

Output Set: N:\CRF4\10122006\J551655A.raw

3 <110> APPLICANT: AYABE, SHIN-ICHI
 4 AKASHI, TOMOYOSHI
 5 AOKI, TOSHIO
 7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE
 8 DEHYDRATASE AND APPLICATION OF THE SAME
 10 <130> FILE REFERENCE: 8062-1031
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/551,655A
 13 <141> CURRENT FILING DATE: 2005-09-28
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP04/04214
 16 <151> PRIOR FILING DATE: 2004-03-25
 18 <150> PRIOR APPLICATION NUMBER: JP 2003-092337
 19 <151> PRIOR FILING DATE: 2003-03-28
 21 <160> NUMBER OF SEQ ID NOS: 10
 23 <170> SOFTWARE: PatentIn Ver. 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 328
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Glycyrrhiza echinata
 30 <400> SEQUENCE: 1
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 32 1 5 10 15
 34 Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp Gly Thr Val Glu Arg Phe
 35 20 25 30
 37 Leu Gly Ser Ser Phe Val Pro Pro Ser Pro Glu Asp Pro Glu Thr Gly
 38 35 40 45
 40 Val Ser Thr Lys Asp Ile Val Ile Ser Glu Asn Pro Thr Ile Ser Ala
 41 50 55 60
 43 Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr Thr Glu Lys Leu Pro Ile
 44 65 70 75 80
 46 Leu Val Tyr Tyr His Gly Gly Ala Phe Cys Leu Glu Ser Ala Phe Ser
 47 85 90 95
 49 Phe Leu His Gln Arg Tyr Leu Asn Ile Val Ala Ser Lys Ala Asn Val
 50 100 105 110
 52 Leu Val Val Ser Ile Glu Tyr Arg Leu Ala Pro Glu His Pro Leu Pro
 53 115 120 125
 55 Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu Lys Trp Val Thr Ser His
 56 130 135 140
 58 Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala Asp Pro Trp Leu Ile Lys
 59 145 150 155 160
 61 His Gly Asp Phe Asn Arg Phe Tyr Ile Gly Gly Asp Thr Ser Gly Ala
 62 165 170 175
 64 Asn Ile Ala His Asn Ala Ala Leu Arg Val Gly Ala Glu Ala Leu Pro
 65 180 185 190

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67 Gly Gly Leu Arg Ile Ala Gly Val Leu Ser Ala Phe Pro Leu Phe Trp
68      195                200                205
70 Gly Ser Lys Pro Val Leu Ser Glu Pro Val Glu Gly His Glu Lys Ser
71      210                215                220
73 Ser Pro Met Gln Val Trp Asn Phe Val Tyr Pro Asp Ala Pro Gly Gly
74 225      230                235                240
76 Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala Pro Gly Ala Pro Asn Leu
77      245                250                255
79 Ala Thr Leu Gly Cys Pro Lys Met Leu Val Phe Val Ala Gly Lys Asp
80      260                265                270
82 Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr Glu Ala Val Lys Glu Ser
83      275                280                285
85 Gly Trp Lys Gly Asp Val Glu Leu Ala Gln Tyr Glu Gly Glu Glu His
86      290                295                300
88 Cys Phe Gln Ile Tyr His Pro Glu Thr Glu Asn Ser Lys Asp Leu Ile
89 305      310                315                320
91 Gly Arg Ile Ala Ser Phe Leu Val
92      325
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96 <211> LENGTH: 1178
97 <212> TYPE: DNA
98 <213> ORGANISM: Glycyrrhiza echinata
100 <220> FEATURE:
101 <221> NAME/KEY: CDS
102 <222> LOCATION: (23)..(1006)
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107      1                5                10
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110 Lys Glu Ile Asp Arg Glu Leu Pro Pro Leu Leu Arg Val Tyr Lys Asp
111      15                20                25
113 gga acc gtg gag cga ttc cta ggc tca tcg ttt gta cca cct tcc cct 148
114 Gly Thr Val Glu Arg Phe Leu Gly Ser Ser Phe Val Pro Pro Ser Pro
115      30                35                40
117 gaa gac ccc gaa aca ggg gtt tcc acg aaa gac ata gta atc tca gaa 196
118 Glu Asp Pro Glu Thr Gly Val Ser Thr Lys Asp Ile Val Ile Ser Glu
119      45                50                55
121 aac ccc acc atc tct gct cgc gtt tac ctt cca aaa ctg aac aac acc 244
122 Asn Pro Thr Ile Ser Ala Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr
123      60                65                70
125 acc gag aag ctc cca atc ttg gtc tac tac cac ggc ggc gcg ttc tgc 292
126 Thr Glu Lys Leu Pro Ile Leu Val Tyr Tyr His Gly Gly Ala Phe Cys
127 75      80                85                90
129 ctc gaa tct gct ttc tcc ttc ctc cac caa cgc tac ctc aac atc gtt 340
130 Leu Glu Ser Ala Phe Ser Phe Leu His Gln Arg Tyr Leu Asn Ile Val
131      95                100                105
133 gct tcc aag gca aat gtt cta gta gtt tcc atc gag tac agg ctc gcc 388
134 Ala Ser Lys Ala Asn Val Leu Val Val Ser Ile Glu Tyr Arg Leu Ala

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135          110          115          120
137 cca gaa cac cct ctt ccg gct gca tat gaa gat ggt tgg tat gct ctc 436
138 Pro Glu His Pro Leu Pro Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu
139          125          130          135
141 aaa tgg gtc act tct cat tcc aca aac aac aac aaa ccc acc aac gct 484
142 Lys Trp Val Thr Ser His Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala
143          140          145          150
145 gac cca tgg ttg atc aaa cac ggt gat ttc aac agg ttc tac atc ggg 532
146 Asp Pro Trp Leu Ile Lys His Gly Asp Phe Asn Arg Phe Tyr Ile Gly
147 155          160          165          170
149 ggt gac act tct ggt gca aac att gca cac aat gcg gct ctt cgt gtt 580
150 Gly Asp Thr Ser Gly Ala Asn Ile Ala His Asn Ala Ala Leu Arg Val
151          175          180          185
153 ggt gct gag gcc tta cct ggg ggg ctg aga ata gca ggg gta ctc tct 628
154 Gly Ala Glu Ala Leu Pro Gly Gly Leu Arg Ile Ala Gly Val Leu Ser
155          190          195          200
157 gct ttt cct ctg ttt tgg ggt tct aag cct gtt ttg tca gaa cct gtc 676
158 Ala Phe Pro Leu Phe Trp Gly Ser Lys Pro Val Leu Ser Glu Pro Val
159          205          210          215
161 gag ggg cat gag aag agc tca ccc atg caa gtt tgg aac ttt gtg tac 724
162 Glu Gly His Glu Lys Ser Ser Pro Met Gln Val Trp Asn Phe Val Tyr
163          220          225          230
165 cca gat gca cca ggt ggc ata gat aac cca cta atc aac cct ttg gca 772
166 Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala
167 235          240          245          250
169 cct ggg gct cct aac ttg gcc aca ctt ggg tgt cca aag atg ttg gtc 820
170 Pro Gly Ala Pro Asn Leu Ala Thr Leu Gly Cys Pro Lys Met Leu Val
171          255          260          265
173 ttt gtt gcg ggg aag gat gat ctt aga gac aga ggg att tgg tac tat 868
174 Phe Val Ala Gly Lys Asp Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr
175          270          275          280
177 gag gct gtg aag gaa agt ggg tgg aaa ggg gat gtg gaa ctt gct cag 916
178 Glu Ala Val Lys Glu Ser Gly Trp Lys Gly Asp Val Glu Leu Ala Gln
179          285          290          295
181 tat gaa ggg gag gaa cat tgc ttc cag atc tac cat cct gaa act gag 964
182 Tyr Glu Gly Glu Glu His Cys Phe Gln Ile Tyr His Pro Glu Thr Glu
183          300          305          310
185 aat tct aaa gat ctc atc ggt cgc atc gct tcc ttc ctt gtt 1006
186 Asn Ser Lys Asp Leu Ile Gly Arg Ile Ala Ser Phe Leu Val
187 315          320          325
189 tgaacacaca gctagacttc ggggttcatta ttactagtat gtgattttgt ttgattaatg 1066
191 ttttgtcatc aattgatggg taataaattg gattagggtta ctagggttcc tgaatcatgc 1126
193 tcaattttac ttttcctgta ctattacttg tttatgaaag aattaatggc at 1178
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 319
198 <212> TYPE: PRT
199 <213> ORGANISM: Glycine max
201 <400> SEQUENCE: 3
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203      1              5              10              15
205 Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala
206              20              25              30
208 Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile
209              35              40              45
211 Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His
212              50              55              60
214 His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala
215      65              70              75              80
217 Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn
218              85              90              95
220 Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg
221              100             105             110
223 Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr
224              115             120             125
226 Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn
227      130             135             140
229 Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val
230     145             150             155             160
232 Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg
233              165             170             175
235 Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu
236              180             185             190
238 Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala
239              195             200             205
241 Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala
242      210             215             220
244 Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys
245     225             230             235             240
247 Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu
248              245             250             255
250 Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr
251              260             265             270
253 His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe
254              275             280             285
256 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
257      290             295             300
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260     305             310             315
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264 <211> LENGTH: 960
265 <212> TYPE: DNA
266 <213> ORGANISM: Glycine max
268 <220> FEATURE:
269 <221> NAME/KEY: CDS
270 <222> LOCATION: (1)..(957)
272 <400> SEQUENCE: 4
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274 Met Ala Lys Glu Ile Val Lys Glu Leu Leu Pro Leu Ile Arg Val Tyr

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Input Set : A:\80621031.APP

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277	aag gat ggc agc gtg gag cgt ctt cta agc tct gaa aac gtg gca gcc	96			
278	Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala				
279	20 25 30				
281	tcc cct gaa gat ccc caa act gga gtc tca tcc aaa gac ata gtc atc	144			
282	Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile				
283	35 40 45				
285	gca gac aac ccc tac gtc tcc gct cgc att ttc ctt ccc aaa tcc cac	192			
286	Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His				
287	50 55 60				
289	cac act aac aac aaa ctc ccc atc ttc ctc tac ttc cac ggt ggc gcc	240			
290	His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala				
291	65 70 75 80				
293	ttt tgc gtc gaa tcc gcc ttc tcc ttt ttc gtc cac cgc tat ctc aac	288			
294	Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn				
295	85 90 95				
297	atc ttg gcc tca gaa gcc aac ata ata gcc atc tcc gtc gac ttc aga	336			
298	Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg				
299	100 105 110				
301	ctc ctc cca cac cac cct atc cct gct gcc tac gaa gac ggt tgg acc	384			
302	Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr				
303	115 120 125				
305	acc ctc aaa tgg att gct tcc cac gcc aac aac acc aac acc acc aac	432			
306	Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn				
307	130 135 140				
309	ccg gag cca tgg cta ctc aac cac gcc gac ttc acc aaa gtc tac gta	480			
310	Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val				
311	145 150 155 160				
313	gga ggt gaa acc agc ggt gct aac atc gca cac aac ctg ctt ttg cgt	528			
314	Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg				
315	165 170 175				
317	gca ggt aac gaa tcc ctc ccc ggg gat ctg aaa ata ttg ggt gga tta	576			
318	Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu				
319	180 185 190				
321	cta tgc tgc ccc ttc ttc tgg ggc tcg aag cca att ggg tcg gag gct	624			
322	Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala				
323	195 200 205				
325	gtt gag ggg cac gag cag agt ttg gcc atg aag gtc tgg aac ttt gcc	672			
326	Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala				
327	210 215 220				
329	tgc cct gat gcc ccc ggt gga atc gat aac ccc tgg atc aac ccc tgt	720			
330	Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys				
331	225 230 235 240				
333	gtt cct ggg gca ccc tct ttg gcc act ctt gcc tgc tct aag ttg ctc	768			
334	Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu				
335	245 250 255				
337	gtt act atc act ggc aaa gac gag ttc aga gac aga gat att ctc tac	816			
338	Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr				
339	260 265 270				

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/551,655A

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TIME: 09:38:16

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number